

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: JULIUS, Michael H.; FILIPP, Dominik;
ALIZADEH-KHIAVI, Kamel

(ii) TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
PROTEIN (CD14), ENCODING GENE AND
APPLICATION
IN B CELL ACTIVATION

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Torys LLP (Customer No. 33721)
(B) STREET: Suite 3000, 79 Wellington Street West, Box 270
(C) CITY: Toronto
(D) PROVINCE: Ontario
(E) COUNTRY: Canada
(F) ZIP: M5K 1N2

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
(B) COMPUTER: COMPAQ, IBM PC compatible
(C) OPERATING SYSTEM: MS-DOS 5.1
(D) SOFTWARE: WORD PERFECT

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/313,177
(B) FILING DATE: May 18, 1999

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBERS: 08/746,883; PCT/CA 97/00880
(B) FILING DATE: November 18, 1996; November 18, 1997

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGGTGTGCG TGCCCTACCT GCTGCTGCTG CTGCTGCCGT CACTGCTGCG TGTGTCTGCG
60
GACACAACAG AACCTTGGCA GCTGGACGAC GACGATTTC GTTGTGTCTG CAACTTCACG
120
GATCCGAAGC CTGACTGGTC TAGCGCCGTT CAGTGTATGG TTGCCCTCGA GGTGGAGATC
180
AGTGCCGGCG GCCGCAGCCT GGAACAGTTT CTCAAGGGAG CCGACACCAA CCCGAAGCAG
240
TATGCTGACA CAATCAAGGC TCTGCGCGTT CGGCGACTCA AGCTGGGCGC TGCACAGGTT
300
CCTGCTCAGC TTCTGGTCGC CGTTCTGCCG GCGCTCGGGT ACTCTCGTCT CAAGGAACTG
360
ACGCTTGAGG ACCTGGAGGT AACCGGCCCA ACGCCCCCGA CGCCTCTGGA AGCCGCTGGG
420
CCTGCGCTCA CCACCCTCAG TCTGCGTAAC GTATCGTGGA CAACAGGAGG TGCCTGGSCT
480
GGCGAACTGC AGCAGTGGCT CAAGCCTGGG CTCAGGGTGC TGAACATTGC CCAAGCACAC
540
TCGCTTGCCCT TTCCGTGCGC AGGGCTCTCC ACCTTCGAGG CGCTCACCAC CCTAGACCTG
600
TCTGACAATC CCAGTCTCGG CGACACGGGG CTGATGGCAG CTCTCTGTCC GAACAAGTTC
660
CCGCCCCCTC AATATCTAGC GCTACGCAAC GCGGGGATGG AGACGCCGAG CGGCGTGTGC
720
GCGGCGCTGG CGGCAGCGAG GGTGCAGCCC CAAAGCCTGG ACCTCAGCCA CAACTCGCTG
780
CGCGTCAACG CCCCCGGTGC TACCCGATGT GTCTGGCCCA GTGACTAAG GTCTCTCAAT
840
TTGTCGTTTC CTGGGCTGGA GCAAGTGCCT AAGGGACTGC CCCCTAAGCT CAGCGTGCTT
900

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GATCTCAGCT GCAACAAGCT AAGCAGGGAG CCGCGGCGAG ACGAGCTGCC CGAGGTAAAT
960

GACCTGACTC TGGACGGAAA TCCCTTTCTG GACCCTGGAG CCCTCCAGCA CCAAAATGAC
1020

CCGATGATCT CCGGCGTGGT CCCAGCCTGT GCGCGTTCTG CCTTGACCAT GGGGGTGTCA
1080

GGAGCCCTGG CGCTGCTTCA AGGAGCCCGA GGCTTCGCGT AA
1122

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGAGCGCG CGTCCTGCTT GTTGCTGCTG CTGCTGCCGC TGGTGACGT CTCTGCGACC
60

ACGCCAGAAC CTTGTGAGCT GGACGATGAA GATTTCGGCT GCGTCTGCAA CTTCTCCGAA
120

CCTCAGCCCG ACTGGTCCGA AGCCTTCCAG TGTGTGTCTG CAGTAGAGGT GGAGATCCAT
180

GGCGGCGGTC TCAACCTAGA GCCGTTTCTA AAGCGCGTCG ATGCGGACGC CGACCCGCGG
240

CAGTATGCTG ACACGGTCAA GGCTCTCCGC GTGCGGCGGC TCACAGTGGG AGCCGCACAG
300

GTTCTGCTC AGCTACTGGT AGGCGCCCTG CGTGTGCTAG CGTACTCCCG CCTCAAGGAA
360

CTGACGCTCG AGGACCTAAA GATAACCGGC ACCATGCCTC CGCTGCCTCT GGAAGCCACA
420

GGACTTGAC TTTCCAGCTT GCGCCTACGC AACGTGTCGT GGGCGACAGG GCGTTCTTGG
480

CTCGCCGAGC TGCAGCAGTG GCTCAAGCCA GGCCTCAAGG TACTGAGCAT TGCCCAAGCA
540

CACTCGCCTG CCTTTTCTG CGAACAGGTT CGCGCCTTCC CGGCCCTTAC CAGCCTAGAC
600

CTGTCTGACA ATCCTGGACT GGGCGAACGC GGAATGATGG CGGCTCTCTG TCCCCACAAG
660

TTCCCGGCCA TCCAGAATCT AGCGCTGCGC AACACAGGAA TGGAGACGCC CACAGGCGTG
720

TGCGCCGCAC TGGCGGCGGC AGGTGTGCAG CCCACAGCC TAGACCTCAG CCACAACTCG
780

CTGCCCGCCA CCGTAAACCC TAGCGCTCCG AGATGCATGT GGTCCAGCGC CCTGAACTCC
840

CTCAATCTGT CGTTCGCTGG GCTGGAACAG GTGCCTAAAG GACTGCCAGC CAAGCTCAGA
900

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GTGCTCGATC TCAGCTGCAA CAGACTGAAC AGGGCGCCGC AGCCTGACGA GCTCCCCGAG
960

GTGGATAACC TGACACTGGA CGGGAATCCC TTCCTGGTCC CTGGAACTGC CCTCCCCAC
1020

GAGGGCTCAA TGAACCTCCG CGTGGTCCCA GCCTGTGCAC GTTCGACCCT GTCGGTGGG
1080

GTGTCGGGAA CCCTGGTGCT GCTCCAAGGG GCCCGGGGCT TTGCCTAA
1128

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGGAGCGTG TGCTTGGCTT GTTGCTGTTG CTTCTGGTGC ACGCCTCTCC CGCCCCACCA
60

GAGCCCTGCG AGCTAGACGA GGAAAGTTGT TCCTGCAACT TCTCAGATCC GAAGCCAGAT
120

TGGTCCAGCG CTTTCAATTG TTTGGGGGCG GCAGATGTGG AATTGTACGG CGGCGGCCCG
180

AGCCTGGAAT ACCTTCTAAA GCGTGTGGAC ACGGAAGCAG ATCTGGGGCA GTTCACTGAT
240

ATTATCAAGT CTCTGTCCCT AAAGCGGCTT ACGGTGCGGG CCGCGCGGAT TCCTAGTCGG
300

ATTCTATTCC GAGCCCTGCG TGTGCTCGGG ATTTCCGGCC TCCAGGAACT GACTCTTGAA
360

AATCTCGAGG TAACCGGCAC CGCGCCGCCA CCGCTTCTGG AAGCCACCGG ACCCGATCTC
420

AACATCTTGA ACCTCCGCAA CGTGTCGTGG GCAACAAGGG ATGCCTGGCT CGCAGAACTG
480

CAGCAGTGGC TAAAGCCTGG ACTCAAGGTA CTGAGTATTG CCCAAGCACA CTCACTCAAC
540

TTTTCTGCG AACAGGTCCG CGTCTTCCCT GCCCTCTCCA CCTTAGACCT GTCTGACAAT
600

CCTGAATTGG GCGAGAGAGG ACTGATCTCA GCCCTCTGTC CCCTCAAGTT CCCGACCCTC
660

CAAGTTTTAG CGCTGCGTAA CGCGGGGATG GAGACGCCCA GCGGCGTGTG CTCTGCGCTG
720

GCCGCAGCAA GGTACAGCT GCAAGGACTA GACCTTAGTC ACAATTCAC T GCGGGATGCT
780

GCAGGCGCTC CGAGTTGTGA CTGGCCCAGT CAGCTAAACT CGCTCAATCT GTCTTTCACT
840

GGGCTGAAGC AGGTACCTAA AGGGCTGCCA GCCAAGCTCA GCGTGCTGGA TCTCAGTTAC
900

AACAGGCTGG ATAGGAACCC TAGCCCAGAT GAGCTGCCCC AAGTGGGGAA CCTGTCACTT
960

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AAAGGAAATC CCTTTTGGG CTCTGAATCC CACTCGGAGA AGTTTAACTC TGGCGTAGTC
1020

ACCGCCGGAG CTCCATCATC CCAAGCAGTG GCCTTGTCAG GAACTCTGGC TTGCTCCTA
1080

GGAGATCGCC TCTTTGTTTA A
1101

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(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Cys	Val	Pro	Tyr	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Ser	Leu	Leu	1	5	10	15
Arg	Val	Ser	Ala	Asp	Thr	Thr	Glu	Pro	Cys	Glu	Leu	Asp	Asp	Asp	Asp	20	25	30	
Phe	Arg	Cys	Val	Cys	Asn	Phe	Thr	Asp	Pro	Lys	Pro	Asp	Trp	Ser	Ser	35	40	45	
Ala	Val	Gln	Cys	Met	Val	Ala	Val	Glu	Val	Glu	Ile	Ser	Ala	Gly	Gly	50	55	60	
Arg	Ser	Leu	Glu	Gln	Phe	Leu	Lys	Gly	Ala	Asp	Thr	Asn	Pro	Lys	Gln	65	70	75	80
Tyr	Ala	Asp	Thr	Ile	Lys	Ala	Leu	Arg	Val	Arg	Arg	Leu	Lys	Leu	Gly	85	90	95	
Ala	Ala	Gln	Val	Pro	Ala	Gln	Leu	Leu	Val	Ala	Val	Leu	Arg	Ala	Leu	100	105	110	
Gly	Tyr	Ser	Arg	Leu	Lys	Glu	Leu	Thr	Leu	Glu	Asp	Leu	Glu	Val	Thr	115	120	125	
Gly	Pro	Thr	Pro	Pro	Thr	Pro	Leu	Glu	Ala	Ala	Gly	Pro	Ala	Leu	Thr	130	135	140	
Thr	Leu	Ser	Leu	Arg	Asn	Val	Ser	Trp	Thr	Thr	Gly	Gly	Ala	Trp	Leu	145	150	155	160
Gly	Glu	Leu	Gln	Gln	Trp	Leu	Lys	Pro	Gly	Leu	Arg	Val	Leu	Asn	Ile	165	170	175	
Ala	Gln	Ala	His	Ser	Leu	Ala	Phe	Pro	Cys	Ala	Gly	Leu	Ser	Thr	Phe	180	185	190	
Glu	Ala	Leu	Thr	Thr	Leu	Asp	Leu	Ser	Asp	Asn	Pro	Ser	Leu	Gly	Asp	195	200	205	
Thr	Gly	Leu	Met	Ala	Ala	Leu	Cys	Pro	Asn	Lys	Phe	Pro	Ala	Leu	Gln	210	215	220	
Tyr	Leu	Ala	Leu	Arg	Asn	Ala	Gly	Met	Glu	Thr	Pro	Ser	Gly	Val	Cys	225	230	235	240

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Ala Ala Leu Ala Ala Ala Arg Val Gln Pro Gln Ser Leu Asp Leu Ser
245 250 255

His Asn Ser Leu Arg Val Thr Ala Pro Gly Ala Thr Arg Cys Val Trp
260 265 270

Pro Ser Ala Leu Arg Ser Leu Asn Leu Ser Phe Ala Gly Leu Glu Gln
275 280 285

Val Pro Lys Gly Leu Pro Pro Lys Leu Ser Val Leu Asp Leu Ser Cys
290 295 300

Asn Lys Leu Ser Arg Glu Pro Arg Arg Asp Glu Leu Pro Glu Val Asn
305 310 315 320

Asp Leu Thr Leu Asp Gly Asn Pro Phe Leu Asp Pro Gly Ala Leu Gln
325 330 335

His Gln Asn Asp Pro Met Ile Ser Gly Val Val Pro Ala Cys Ala Arg
340 345 350

Ser Ala Leu Thr Met Gly Val Ser Gly Ala Leu Ala Leu Leu Gln Gly
355 360 365

Ala Arg Gly Phe Ala
370

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Glu Arg Ala Ser Cys Leu Leu Leu Leu Leu Leu Pro Leu Val His
1 5 10 15

Val Ser Ala Thr Thr Pro Glu Pro Cys Glu Leu Asp Asp Glu Asp Phe
20 25 30

Arg Cys Val Cys Asn Phe Ser Glu Pro Gln Pro Asp Trp Ser Glu Ala
35 40 45

Phe Gln Cys Val Ser Ala Val Glu Val Glu Ile His Ala Gly Gly Leu
50 55 60

Asn Leu Glu Pro Phe Leu Lys Arg Val Asp Ala Asp Ala Asp Pro Arg
65 70 75 80

Gln Tyr Ala Asp Thr Val Lys Ala Leu Arg Val Arg Arg Leu Thr Val
85 90 95

Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val
100 105 110

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(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Glu	Arg	Val	Leu	Gly	Leu	Leu	Leu	Leu	Leu	Val	His	Ala	Ser	1	5	10	15
Pro	Ala	Pro	Pro	Glu	Pro	Cys	Glu	Leu	Asp	Glu	Glu	Ser	Cys	Ser	Cys	20	25	30
Asn	Phe	Ser	Asp	Pro	Lys	Pro	Asp	Trp	Ser	Ser	Ala	Phe	Asn	Cys	Leu	35	40	45
Gly	Ala	Ala	Asp	Val	Glu	Leu	Tyr	Gly	Gly	Gly	Arg	Ser	Leu	Glu	Tyr	50	55	60
Leu	Leu	Lys	Arg	Val	Asp	Thr	Glu	Ala	Asp	Leu	Gly	Gln	Phe	Thr	Asp	65	70	75
Ile	Ile	Lys	Ser	Leu	Ser	Leu	Lys	Arg	Leu	Thr	Val	Arg	Ala	Ala	Arg	85	90	95
Ile	Pro	Ser	Arg	Ile	Leu	Phe	Gly	Ala	Leu	Arg	Val	Leu	Gly	Ile	Ser	100	105	110
Gly	Leu	Gln	Glu	Leu	Thr	Leu	Glu	Asn	Leu	Glu	Val	Thr	Gly	Thr	Ala	115	120	125
Pro	Pro	Pro	Leu	Leu	Glu	Ala	Thr	Gly	Pro	Asp	Leu	Asn	Ile	Leu	Asn	130	135	140
Leu	Arg	Asn	Val	Ser	Trp	Ala	Thr	Arg	Asp	Ala	Trp	Leu	Ala	Glu	Leu	145	150	155
Gln	Gln	Trp	Leu	Lys	Pro	Gly	Leu	Lys	Val	Leu	Ser	Ile	Ala	Gln	Ala	165	170	175
His	Ser	Leu	Asn	Phe	Ser	Cys	Glu	Gln	Val	Arg	Val	Phe	Pro	Ala	Leu	180	185	190
Ser	Thr	Leu	Asp	Leu	Ser	Asp	Asn	Pro	Glu	Leu	Gly	Glu	Arg	Gly	Leu	195	200	205
Ile	Ser	Ala	Leu	Cys	Pro	Leu	Lys	Phe	Pro	Thr	Leu	Gln	Val	Leu	Ala	210	215	220
Leu	Arg	Asn	Ala	Gly	Met	Glu	Thr	Pro	Ser	Gly	Val	Cys	Ser	Ala	Leu	225	230	235
Ala	Ala	Ala	Arg	Val	Gln	Leu	Gln	Gly	Leu	Asp	Leu	Ser	His	Asn	Ser	245	250	255

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Leu Arg Asp Ala Ala Gly Ala Pro Ser Cys Asp Trp Pro Ser Gln Leu
260 265 270

Asn Ser Leu Asn Leu Ser Phe Thr Gly Leu Lys Gln Val Pro Lys Gly
275 280 285

Leu Pro Ala Lys Leu Ser Val Leu Asp Leu Ser Tyr Asn Arg Leu Asp
290 295 300

Arg Asn Pro Ser Pro Asp Glu Leu Pro Gln Val Gly Asn Leu Ser Leu
305 310 315 320

Lys Gly Asn Pro Phe Leu Asp Ser Glu Ser His Ser Glu Lys Phe Asn
325 330 335

Ser Gly Val Val Thr Ala Gly Ala Pro Ser Ser Gln Ala Val Ala Leu
340 345 350

Ser Gly Thr Leu Ala Leu Leu Leu Gly Asp Arg Leu Phe Val
355 360 365

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCTAGCGCTA GCCACCATGG TGTGCGTGCC CTACCTGCT
39

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTAGCGCTA GCCGCGAAGC CTCGGGCTCC TTGAAG
36

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- (2) INFORMATION FOR SEQ ID NO: 9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTCGAGCTCG AGGCTAGCCA CCATGGTGTG CGTGCC
36

- (2) INFORMATION FOR SEQ ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCGAGCTGA GGGATCCCTA AGCGTAATCT GGAAC
35

- (2) INFORMATION FOR SEQ ID NO: 11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTAGAATTCT CTCCCGCCCC ACCAGAGCCC TGCG
34

- (2) INFORMATION FOR SEQ ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTAGAATTCT TAAACAAAGA GGCGATCTCC TAGG
34

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TACCAATACG ATGTTCCAGA TTACGCTTAG
30

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GCAGTCGACA CTATAGAATA CTCAAGC
27

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TTCGTCGACA TTGGGCCCTC TAGA